

SEQUENCE LISTING

(1) GENERAL INFORMATION

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(i) APPLICANT: DEEN, KEITH C
YOUNG, PETER R

(ii) TITLE OF THE INVENTION: TUMOR NECROSIS FACTOR RELATED
RECEPTOR, TR6

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(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

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(A) ADDRESSEE: RATNER & PRESTIA

(B) STREET: P.O. BOX 980

(C) CITY: VALLEY FORGE

(D) STATE: PA

(E) COUNTRY: USA

(F) ZIP: 19482

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

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(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED

(B) FILING DATE: 09-MAY-1997

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(C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/041,230

(B) FILING DATE: 14-MAR-1997

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(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: PRESTIA, PAUL F.
 (B) REGISTRATION NUMBER: 23,031
 (C) REFERENCE/DOCKET NUMBER: GH-50008

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-407-0700
 (B) TELEFAX: 610-407-0701
 (C) TELEX: 846169

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3,881 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTTTGCGCCC ACAAATACA CCGACGATGC CCGATCTACT TTAAGGGCTG AAACCCACGG 60
 GCCTGAGAGA CTATAAGAGC GTTCCCTACC GCCATGGAAC AACGGGGACA GAACGCCCCG 120
 GCCGCTTCGG GGGCCCGGAA AAGGCACGGC CCAGGACCCA GGGAGGCGCG GGGAGCCAGG 180
 CCTGGGCCCC GGGTCCCCAA GACCCCTTGTG CTCGTTGTG CCGCGGTCCT GCTGTTGGTC 240
 TCAGCTGAGT CTGCTCTGAT CACCCAACAA GACCTAGCTC CCCAGCAGAG AGCGGCCCCA 300
 CAACAAAAGA GGTCCAGCCC CTCAGAGGGA TTGTGTCCAC CTGGACACCA TATCTCAGAA 360
 GACGGTAGAG ATTGCATCTC CTGCAAATAT GGACAGGACT ATAGCACTCA ATGGAATGAC 420
 CTCCTTTTCT GCTTGCCTG CACCAGGTGT GATTTCAGGTG AAGTGGAGCT AAGTCCCTGC 480
 ACCACGACCA GAAACACAGT GTGTCAGTGC GAAGAAGGCA CCTTCCGGGA AGAAGATTCT 540
 CCTGAGATGT GCCGGAAGTG CCGCACAGGG TGTCCCAGAG GGATGGTCAA GGTCCGTGAT 600
 TGTACACCTT GGAGTGACAT CGAATGTGTC CACAAAGAAT CAGGCATCAT CATAGGAGTC 660
 ACAGTTGCAG CCGTAGTCTT GATTGTGGCT GTGTTTGTTC GCAAGTCTTT ACTGTGGAAG 720
 AAAGTCCTTC CTTACCTGAA AGGCATCTGC TCAGGTGGTG GTGGGGACCC TGAGCGTGTG 780

	GACAGAAGCT	CACAACGACC	TGGGGCTGAG	GACAATGTCC	TCAATGAGAT	CGTGAGTATC	840
	TTGCAGCCCA	CCCAGGTCCC	TGAGCAGGAA	ATGGAAGTCC	AGGAGCCAGC	AGAGCCCAACA	900
	GGTGTCAACA	TGTTGTCCCC	CGGGGAGTCA	GAGCATCTGC	TGGAACCGGC	AGAAGCTGAA	960
	AGGTCTCAGA	GGAGGAGGCT	GCTGGTTCCA	GCAAATGAAG	GTGATCCAC	TGAGACTCTG	1020
5	AGACAGTGCT	TCGATGACTT	TGCAGACTTG	GTGCCCTTTG	ACTCCTGGGA	GCCGCTCATG	1080
	AGGAAGTTGG	GCCTCATGGA	CAATGAGATA	AAGGTGGCTA	AAGCTGAGGC	AGCGGGCCAC	1140
	AGGGACACCT	TGTACACGAT	GCTGATAAAG	TGGGTCAACA	AAACCGGGCG	AGATGCCTCT	1200
	GTCCACACCC	TGCTGGATGC	CTTGGAGACG	CTGGGAGAGA	GACTTGCCAA	GCAGAAGATT	1260
	GAGGACCACT	TGTTGAGCTC	TGGAAAGTTC	ATGTATCTAG	AAGGTAATGC	AGACTCTGCC	1320
10	ATGTCCTAAG	TGTGATTCTC	TTCAGGAAGT	CAGACCTTCC	CTGGTTTACC	TTTTTTCTGG	1380
	AAAAAGCCCA	ACTGGACTCC	AGTCAGTAGG	AAAGTGCCAC	AATTGTCACA	TGACCGGTAC	1440
	TGGAAGAAAC	TCTCCCATCC	AACATCACCC	AGTGGATGGA	ACATCCTGTA	ACTTTTCACT	1500
	GCACTTGGCA	TTATTTTTAT	AAGCTGAATG	TGATAATAAG	GACACTATGG	AAATGTCTGG	1560
	ATCATTCCGT	TTGTGCGTAC	TTTGAGATTT	GGTTTGGGAT	GTCATTGTTT	TCACAGCACT	1620
15	TTTTTATCCT	AATGTAAATG	CTTTATTTAT	TTATTTGGGC	TACATTGTAA	GATCCATCTA	1680
	CACAGTCGTT	GTCCGACTTC	ACTTGATACT	ATATGATATG	AACCTTTTTT	GGGTGGGGGG	1740
	TGCGGGGCAG	TTCACTCTGT	CTCCAGGCT	GGAGTGCAAT	GGTGCAATCT	TGGCTCACTA	1800
	TAGCCTTGAC	CTCTCAGGCT	CAAGCGATTG	TCCCACCTCA	GCCATCCAAA	TAGCTGGGAC	1860
	CACAGGTGTG	CACCACCACG	CCCGGCTAAT	TTTTTGTATT	TTGTCTAGAT	ATAGGGGCTC	1920
20	TCTATGTTGC	TCAGGGTGGT	CTCGAATTCC	TGGACTCAAG	CAGTCTGCCC	ACCTCAGACT	1980
	CCCAAAGCGG	TGGAATTAGA	GGCGTGAGCC	CCCATGCTTG	GCCTTACCTT	TCTACTTTTA	2040
	TAATTCGTGA	TGTTATTATT	TTATGAACAT	GAAGAAACTT	TAGTAAATGT	ACTTGTTTAC	2100
	ATAGTTATGT	GAATAGATTA	GATAAACATA	AAAGGAGGAG	ACATACAATG	GGGGAAGAAG	2160
	AAGAAGTCCC	CTGTAAGATG	TCACTGTCTG	GGTTCCAGCC	CTCCCTCAGA	TGTACTTTGG	2220
25	CTTCAATGAT	TGGCAACTTC	TACAGGGGCC	AGTCTTTTGA	ACTGGACAAC	CTTACAAGTA	2280
	TATGAGTATT	ATTTATAGGT	AGTTGTTTAC	ATATGAGTCG	GGACCAAAGA	GAACCTGGATC	2340
	CACGTGAAGT	CCTGTGTGTG	GCTGGTCCCT	ACCTGGGCAG	TCTCATTTGC	ACCCATAGCC	2400
	CCCATCTATG	GACAGGCTGG	GACAGAGGCA	GATGGGTTAG	ATCACACATA	ACAATAGGGT	2460
	CTATGTCTATA	TCCCAAGTGA	ACTTGAGCCC	TGTTTGGGCT	CAGGAGATAG	AAGACAAAAT	2520
30	CTGTCTCCCC	ACGTCTGCCA	TGGCATCAAG	GGGGAAGAGT	AGATGGTGCT	TGAGAATGGT	2580
	GTGAAATGGT	TGCCATCTCA	GGAGTAGATG	GCCCCGCTCA	CTTCTGGTTA	TCTGTCACCC	2640
	TGAGCCCATG	AGCTGCCCTT	TAGGGTACAG	ATTGCCTACT	TGAGGACCTT	GGCCGCTCTG	2700
	TAAGCATCTG	ACTCATCTCA	GAAATGTCAA	TTCTTAAACA	CTGTGGCAAC	AGGACCTAGA	2760
	ATGGCTGACG	CATTAAAGTT	TTCTTCTTGT	GTCCGTCTCT	ATTATGTGTT	TAAGACCTCA	2820
35	GTAACCATTT	CAGCCTCTTT	CCAGCAAACC	CTTCTCCATA	GTATTTTCAGT	CATGGAAGGA	2880
	TCATTTATGC	AGGTAGTCAT	TCCAGGAGTT	TTTGGTCTTT	TCTGTCTCAA	GGCATTTGTG	2940

GTTTTGTTC GGGACTGGTT TGGGTGGGAC AAAGTTAGAA TTGCCTGAAG ATCACACATT 3000
 CAGACTGTTG TGTCTGTGGA GTTTTAGGAG TGGGGGGTGA CCTTTCTGGT CTTTGCACCT 3060
 CCATCCTCTC CCACTTCCAT CTGGCATCCC CACGCGTTGT CCCCTGCACT TCTGGAAGGC 3120
 ACAGGGTGCT GCTGCTTCCT GGTCTTTGCC TTTGCTGGGC CTTCTGTGCA GGACGCTCAG 3180
 5 CCTCAGGGCT CAGAAGGTGC CAGTCCGGTC CCAGGTCCCT TGTCCCTTCC ACAGAGGCCT 3240
 TCCTAGAAGA TGCATCTAGA GTGTCAGCCT TATCAGTGT TAAGATTTTT CTTTATTTTT 3300
 TAATTTTTTT GAGACAGAAT CTCACTCTCT CGCCCAGGCT GGAGTGCAAC GGTACGATCT 3360
 TGGCTCAGTG CAACCTCCGC CTCCTGGGTT CAAGCGATTC TCGTGCTCA GCCTCCGGAG 3420
 TAGCTGGGAT TGCAGGCACC CGCCACCACG CCTGGCTAAT TTTTGTATTT TTAGTAGAGA 3480
 10 CGGGGTTTCA CCATGTTGGT CAGGCTGGTC TCGAACTCCT GACCTCAGGT GATCCACNTT 3540
 GGCTCCGAA AGTGCTGGGA TATACAAGGC GTGAGCCACC AGCCAGGCCA AGATATTNTT 3600
 NTAAAGNNAG CTTCCGGANG ACATGAAATA ANGGGGGGTT TTGTTGTTTA GTAACATTNG 3660
 GCTTTGATAT ATCCCCAGGC CAAATNGCAN GNGACACAGG ACAGCCATAG TATAGTGTGT 3720
 CACTCGTGGT TGGTGTCTT TCATGGTTCT GCCCTGTCAA AGGTCCCTAT TTGAAATGTG 3780
 15 TTATAATACA AACAAGGAAG CACATTGTGT ACAAATACT TATGTATTTA TGAATCCATG 3840
 ACCAAATTAA ATATGAAACC TTATATAAAA AAAAAAAAAA A 3881

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
 1 5 10 15
 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
 20 25 30
 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
 35 40 45
 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 50 55 60

Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 65 70 75 80
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 85 90 95
 5 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr Gln Trp Asn Asp Leu Leu Phe
 100 105 110
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 115 120 125
 10 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 130 135 140
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 145 150 155 160
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 165 170 175
 15 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
 180 185 190
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
 195 200 205
 20 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
 210 215 220
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
 225 230 235 240
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
 245 250 255
 25 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
 260 265 270
 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 275 280 285
 30 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
 290 295 300
 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
 305 310 315 320
 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
 325 330 335
 35 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
 340 345 350
 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
 355 360 365
 40 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
 370 375 380
 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
 385 390 395 400

Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser End
405 410 411

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1062 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATGACCTCCT	TTTCTGCTTG	CGCTGCACCA	GGTGTGATTC	AGGTGAAGTG	GAGCTAAGTC	60
CCTGCACCAC	GACCAGAAAC	ACAGTGTGTC	AGTGCGAAGA	AGGCACCTTC	CGGGAAGAAG	120
ATTCTCCTGA	GATGTGCCGG	AAGTGCCGCA	CAGGGTGTCC	CAGAGGGATG	GTCAAGGTCG	180
GTGATTGTAC	ACCCTGGAGT	GACATCGAAT	GTGTCCACAA	AGAATCAGGC	ATCATCATAG	240
GAGTCACAGT	TGCAGCCGTA	GTCTTGATTG	TGGCTGTGTT	TGTTTGCAAG	TCTTTACTGT	300
GGAAGAAAGT	CCTTCCTTAC	CTGAAAGGCA	TCTGCTCAGG	TGGTGGTGGG	GACCCTGAGC	360
GTGTGGACAG	AAGCTCACAA	CGACCTGGGG	CTGAGGACAA	TGTCCTCAAT	GAGATCGTGA	420
GTATCTTGCA	GCCCAACCAG	GTCCCTGAGC	AGGAAATGGA	AGTCCAGGAG	CCAGCAGAGC	480
CAACAGGTGT	CAACATGTTG	TCCCCGGGG	AGTCAGAGCA	TCTGCTGGAA	CCGGCAGAAG	540
CTGAAAGGTC	TCAGAGGAGG	AGGCTGCTGG	TTCCAGCAAA	TGAAGGTGAT	CCCACTGAGA	600
CTCTGAGACA	GTGCTTCGAT	GACTTTGCAG	ACTTGGTGCC	CTTTGACTCC	TGGGAGCCGC	660
TCATGAGGAA	GTTGGGCCTC	ATGGACAATG	AGATAAAGGT	GGCTAAAGCT	GAGGCAGCGG	720
GCCACAGGGA	CACCTTGTAC	ACGATGCTGA	TAAAGTGGGT	CAACAAAACC	GGGCGAGATG	780
CCTCTGTCCA	CACCCTGCTG	GATGCCCTGG	AGACGCTGGG	AGAGAGACTT	GCCAAGCAGA	840
AGATTGAGGA	CCACTTGTTG	AGCTCTGGAA	AGTTCATGTA	TCTAGAAGGT	AATGCAGACT	900
CTGCCATGTC	CTAAGTGTGA	TTCTCTTCAG	GAAGTCAGAC	CTTCCCTGGT	TTACCTTTTTT	960
TCTGGAAAAA	GCCCAACTGG	ACTCCAGTCA	GTAGGAAAGT	GCCACAATTG	TCACATGACC	1020
GGTACTGGAA	GAAACTCTCC	CATCCAACAT	CACCCAGTGG	AT		1062

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS: single

Gly Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
 290 295 300

15050-1025380